

1/9

Input file Fbh2786c.seq; Output File 2786.trans
 Sequence length 2459

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GC	GC	GC	GC	GC	GC	GC	GC	GC	GC	GC	GC	12	73
E	H	S	P	G	S	G	A	R	R	P	L	H	S
GAG	CAT	TCC	CCC	GGC	AGC	GGC	GGC	GGC	GGC	CTG	CAC	TCC	GGC
V	A	S	A	S	N	F	R	A	F	F	L	L	H
GTG	GCC	TTC	GCC	TCC	AAC	TTC	CGG	GCC	TTT	GAG	CTG	CTG	CAC
A	E	P	G	P	P	G	G	A	G	S	R	G	L
GCT	GAG	TTC	GGG	CCT	CCA	GGG	CCC	GGC	GCA	GGG	AGC	CGG	GAG
L	D	L	R	C	L	E	P	E	G	A	E	L	R
CTG	CAC	GTC	CGC	TGC	CTG	GAG	CCC	GAG	GGC	GCC	GCC	GAG	CTG
C	L	E	V	T	A	A	A	L	R	R	E	R	P
TGC	CTG	GAG	GTG	ACG	GGG	GGG	GGG	CTG	GGG	GGG	GGG	GGG	GGG
A	E	P	V	S	F	T	Y	T	O	P	F	S	H
CGC	GAC	CCC	GTG	ATC	TAC	ACG	CAG	CCT	TTC	TGC	CAC	TAT	GGC
S	F	P	O	P	C	R	A	A	P	R	L	O	V
TCC	TTC	CGC	CGC	CCC	TGC	CGC	GCC	GCC	GAG	CGC	CTC	CAG	GTG
G	E	G	P	G	V	C	N	L	A	P	E	O	T
GGG	GAG	GGA	CCC	GGG	GTT	TGC	TGG	TTC	GCT	CCC	GAG	CAG	ACA
T	Y	Y	T	O	G	O	A	V	L	N	R	A	F
TTC	GTG	TAC	ACC	GAC	GGC	CAG	GCT	GTC	CTA	AAC	CGG	GCC	TTC
P	A	V	K	Y	K	Y	S	A	L	I	E	V	P
CCT	GCT	GTT	AAA	TAC	AAG	TAT	TCA	GCT	CTT	ATT	GAG	GTC	CCA
M	S	A	S	T	N	E	K	R	G	P	N	K	F
ATG	AGT	GCT	AGC	ACC	TGG	GAG	AAG	AGA	GGT	CCA	AAT	AAG	TTC
P	I	P	S	Y	L	I	A	L	A	I	G	D	L
CCC	ATC	CCC	TCC	TAT	CTG	ATA	GCT	TTC	GCC	ATC	GAA	GAT	CTG
P	R	S	R	V	N	A	E	P	C	L	I	D	A
CCC	AGG	AGC	CGG	GTG	TGG	GCT	GAG	CCC	TGC	CTG	ATT	GAT	GCT
G	V	I	E	E	L	A	T	G	B	K	L	F	G
GGG	CTG	ATA	GAA	GAA	TTT	TTC	GCA	ACA	GGA	GAG	AAG	CTT	TTT
R	Y	D	L	L	F	M	P	P	S	F	P	F	G
AGG	TAT	GAC	TTG	CTC	TTC	ATG	CCA	CCG	TCC	TTT	CCA	TTT	GGA
L	T	F	V	T	P	C	L	L	A	G	D	R	S
CTG	ACT	TTT	GTC	ACC	CCC	TGC	CTG	CTA	GCT	GGG	GAC	CGC	TCC
H	E	I	S	H	S	W	F	G	N	L	V	T	N
CAT	GAG	ATC	TCC	CAC	AGT	TGG	TTT	GGG	AAC	CTG	GTC	ACC	AAC
N	L	N	E	G	F	T	M	Y	A	O	R	R	I
TGG	CTC	AAT	GAA	GAT	TTC	ACC	ATG	TAC	GCC	CAG	AGG	ATC	TCC
G	A	Y	T	C	L	E	A	A	T	G	R	A	L
GCT	GCG	TAC	ACC	TGC	TTG	GAG	GCT	GCA	ACG	GGG	GCG	GCT	CTG
I	T	G	E	N	P	L	N	K	L	R	V	K	I
ATC	ACT	GGA	GAG	GAA	ACA	CTC	AAC	AAG	CTC	CGC	GTG	AGG	ATT
P	D	D	T	Y	N	E	T	P	Y	E	K	G	F
COG	GAC	ACC	TAT	AAT	GAG	ACC	CCC	TAC	GAG	AAA	GAT	TTC	TGC
A	H	L	V	G	D	O	D	O	F	D	S	F	L
GCC	CAC	TTG	GTG	GGT	GAT	CAG	GAT	TTT	GAC	ACT	TTT	CTC	AAG
F	K	F	R	S	I	L	A	D	D	F	L	D	E
TTC	AAA	TTC	CGA	AGC	ATC	TTA	GCC	GAT	TTT	CTG	GAC	TTC	TAC

FIG. 1A.

2/9

E L K K K R V D I I P G F E F D R W L N 484
 GAG CTT AAG AAA AAG AGA GTG GAT ATC ATT CCA GGT TTT GAT TTT GAT CGA TGG CTC AAT 1452 1513
 T P G W P P Y L P D L S P G D S L M K P 504
 ACC CCC GGC TGC CCG CCG TAC CTC CCT GAT CTC TCC CCT GGG GAC TCA CTC ATG AAG CCT 1512 1573
 A E E L A O L W A A E E L D M K A I E A 524
 GCT GAA GAG CTA GGC CAA CTG TGG GCA GCC GAG GAG CTG GAC ATG AAG GCC ATT GAA GCC 1572 1633
 V A I S P W K T Y O L V Y F L D K I L O 544
 GTG GCC ATC TCT CCC TGG AAG ACC TAC CAG CTG GTC TAC TTC CTG GAT AAG ATC CTC CAG 1632 1693
 K S P L P P G N V K K L G D T Y P S I S 564
 AAA TCC CCT CTC OCT OCT GGG AAT GTG AAA AAA CTT GGA GAC ACA TAC OCA AGT ATC TCA 1692 1753
 N A R N A E L R L R W G O I V L K N D H 584
 AAT GGC CGG AAT GCA GAG CTC CGG CTG CGA TGG GGC CAA ATC GTC CTT AAG AAC GAC CAC 1752 1813
 Q E D F W K V K E F L H N O G K O K Y T 604
 CAG GAA GAT TTC TGG AAA GTG AAG GAG TTC CTG CAT AAC CAG GGG AAG CAG AAG TAT ACA 1812 1873
 L P L Y H A M M G G S E V A O T L A K E 624
 CTT CGG TAC CAC GCA ATG ATG GGT GGC AGT GAG GTG GCG ACC CTC GCC AAG GAG 1872 1933
 T F A S T A S O L H S N V V N Y V O O I 644
 ACT TTT GCA TCC ACC GCC TCC CAG CTC CAC AGC AAT GTT GTC AAC TAT GTC CAG CAG ATC 1932 1993
 V A P K G S * 651
 GTG GCA CCC AAG GGC AGT TAG 1953
 2011
 AGGCTCGTGTGCATGGCCOCTGCCTCTTCAGGCTCTOCAGGCTTCAGAAATATGTTGTTCCTCCAAATTCCTGTGCC
 TGATCAACTTCCTGGAGTTTATATCCOCTCAGGATAATCTATTCTCTAGCTTAGGTATCTGTGACTCTTGGGCTCTGC
 TCTGGTGGGAACCTTACTTCTCTATAGCCCACTGAGCCCGAGACAGAGAACCCTGCCACAGCTCTCCCGCTACAGGCT
 GCAGGCACTGCAGGCGAGCGGTATTCTCTCCCACTAAGTCTCTGGAAGAAGTGGAGAGACTGATGCTCTTCTT
 TTTCCTCTTCTGCTCTTTTCTCTGCTGATTTTATGCAAGGGCTGGCATTCTGATGCTTCTTTTTCAGGTTTATCC
 TTATTTTAAATAAGTTTTCAGGCAAAATTAATAAAAAAAAAAAAAAAAAAAAA

FIG. 1B.

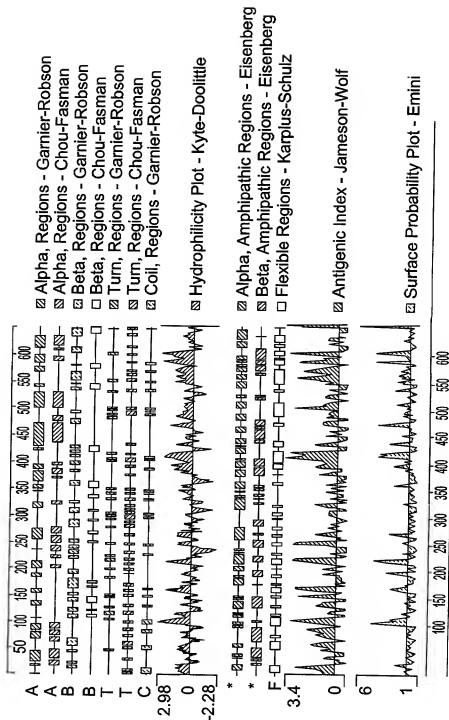


FIG. 2.

Analysis of 2786 (650 aa)

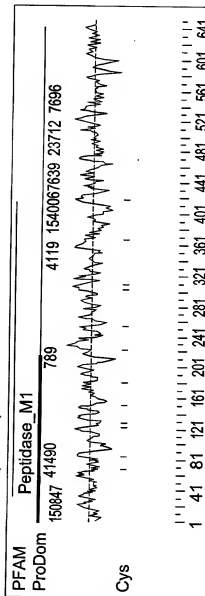


FIG. 3.

5/9

Prosite Pattern Matches for 2786

Prosite version: Release 12.2 of February 1995

>PS00004/PDOC00004/CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 356 RRIS 359

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 141 TYR 143

Query: 374 TGR 376

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 208 STWE 211

Analysis of 2786

Query: 318 SLAD 321

Query: 368 TCLE 371

Query: 386 TGEE 389

Query: 408 TYNE 411

Query: 412 TPYE 415

Query: 496 SPGD 499

>PS00008/PDOC00008/MYRISTYL_N-myristoylation site.

Query: 9 GSGAAR 14

Query: 58 GLSGTA 63

Query: 119 GQALCV 124

Query: 333 GNLVTN 338

Query: 364 GAAATC 369

Query: 614 GSEVAQ 619

>PS00009/PDOC00009/AMIDATION Amidation site.

Query: 159 AGKK 162

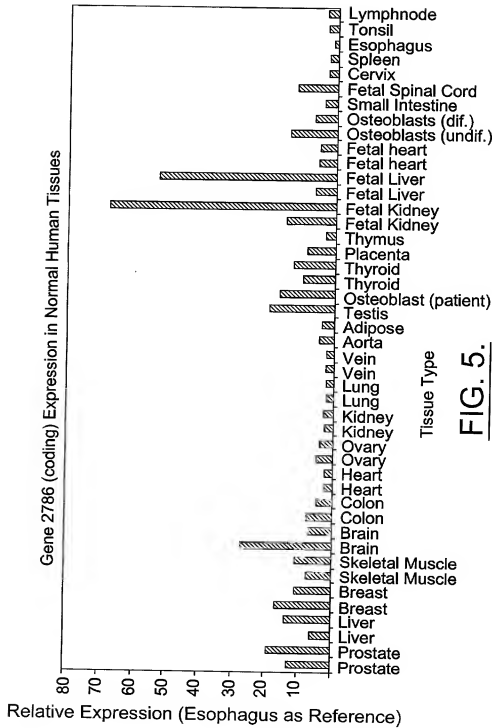
>PS00030/PDOC00030/RNP_1 Eukaryotic putative RNA-binding region RNP-1 signature.

Query: 416 KGFCFVSY 423

>PS00142/PDOC00142/ZINC_PROTEASE Neutral zinc metalloproteases, zinc-binding region signature.

Query: 322 VIIIEISHSW 331

FIG. 4.



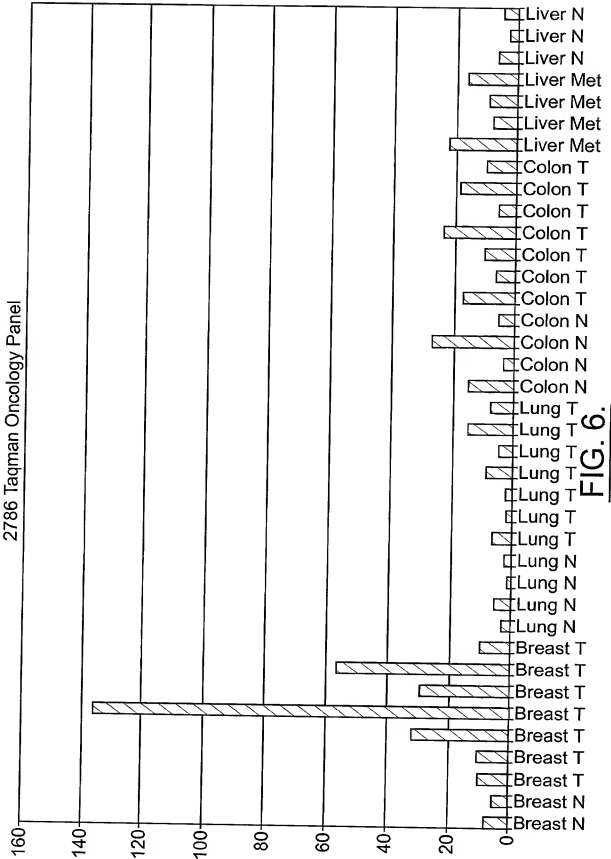


FIG. 6.

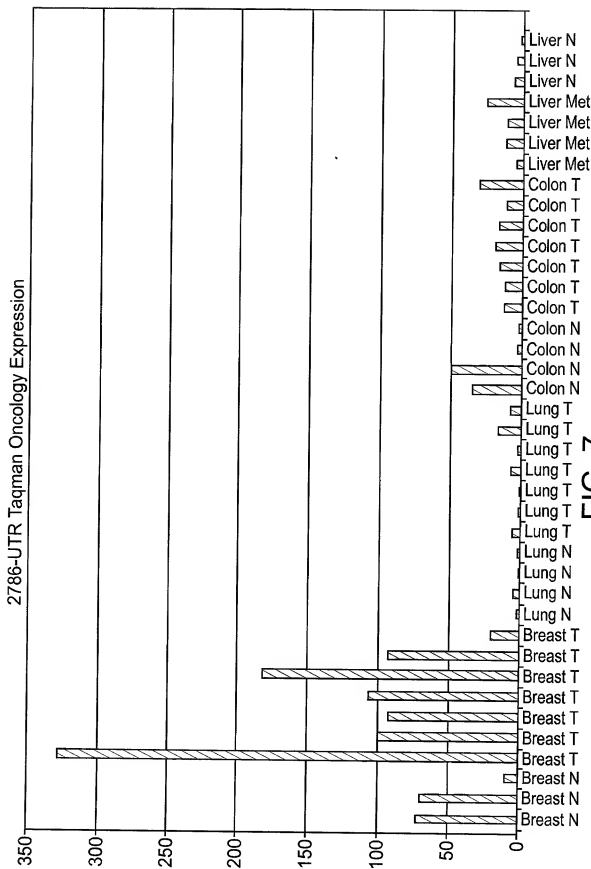


FIG. 7.

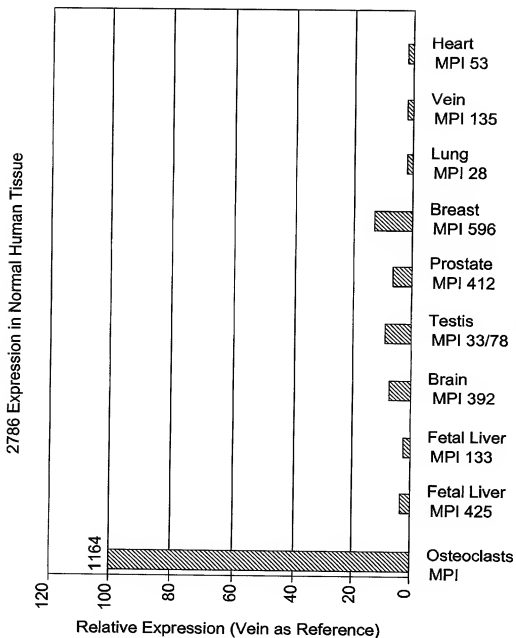


FIG. 8.